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PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In the Application of:

COLDREN ET AL.

CASE NO.: BC1019 US PCT

APPLICATION NO.: 10/069,425

GROUP ART UNIT: UNKNOWN

FILED: FEBRUARY 19, 2002

EXAMINER: UNKNOWN

FOR: CIS-PRENYLTRANSFERASES FROM PLANTS

Assistant Commissioner for Patents  
Washington, DC 20231

Sir:

DECLARATION IN ACCORDANCE WITH 37 CFR 1.821

I hereby state that the content of the paper and computer readable copies of the Sequence Listing, submitted in accordance with 37 CFR 1.821(c) and (e), respectively are the same.

Respectfully submitted,

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Telephone: 302-992-6460

Dated:

*7/26/02*

I hereby certify that this paper is being deposited with the United States Postal Service as First Class Mail in an envelope addressed to: U. S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202 on this date. July 26, 2002

Mary Beth Pitcher

*Mary Beth Pitcher*

SEQUENCE LISTING

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<150> 60/155,046

<151> 1999-09-21

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<213> Dimorphotheca

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<213> Calendula officinalis

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Lys Val Lys Asp Gly Val Ile Ile Pro Lys Gln Ile Asp Glu Lys Tyr
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Phe Lys Gln Glu Leu Gly Thr Lys Met Ile Asp Phe Pro Tyr Pro Asp
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 65 70 75 80  
 Thr Ile Tyr Ala Phe Ser Ile Asp Asn Phe Arg Arg Lys Pro His Glu  
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Ser Tyr Ser Gly Ile Lys Leu Val Asp Leu Glu Lys Asn Thr Tyr Ile  
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Asn Pro Tyr Pro Asp Val Leu Ile Arg Thr Ser Gly Glu Thr Arg Leu  
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Ser Asn Tyr Leu Leu Trp Gln Thr Thr Asn Cys Ile Leu Tyr Ser Pro  
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Tyr Ala Leu Trp Pro Glu Ile Gly Leu Arg His Val Val Trp Ser Val  
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 Lys His Lys Leu Pro Glu Gly Gly Gly His Lys Ala Gly Phe Leu Ala  
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 Val Cys Tyr Thr Ser Thr Asp Glu Ile Val His Ala Val Glu Glu Ser  
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 Ser Tyr Ser Gly Ile Lys Leu Val Asp Leu Glu Lys Asn Thr Tyr Ile  
 210 215 220  
 Asn Pro Tyr Pro Asp Val Leu Ile Arg Thr Ser Gly Glu Thr Arg Leu  
 225 230 235 240  
 Ser Asn Tyr Leu Leu Trp Gln Thr Thr Asn Cys Ile Leu Tyr Ser Pro  
 245 250 255  
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 Ser Phe Ser Phe Pro Pro Ile Ser Val Pro Arg Phe His Lys Leu Arg  
           35                  40                  45  
 Thr Ala Lys Thr Asp Val Val Gly Glu Glu Glu Ala Arg Glu Val Asn  
   50                  55                  60  
 Glu Arg Ala Glu Glu Phe Pro Asp Gly Leu Arg Arg Glu Leu Met Pro  
   65                  70                  75                  80  
 Glu His Val Ala Val Ile Met Asp Gly Asn Val Arg Trp Ala Gln Lys  
           85                  90                  95  
 Arg Gly Leu Pro Ala Ala Ser Gly His Gln Ala Gly Val Arg Ser Leu  
          100                 105                 110  
 Arg Glu Leu Val Glu Leu Cys Cys Lys Trp Gly Ile Lys Val Leu Ser  
  115                 120                 125  
 Val Phe Ala Phe Ser Tyr Asp Asn Trp Ser Arg Ser Glu Gly Glu Val  
  130                 135                 140  
 Gly Phe Leu Met Ser Leu Ile Glu Arg Val Val Lys Ala Glu Leu Pro  
 145                 150                 155                 160  
 Ile Leu Gly Gly Lys Ala Phe Glu Cys Arg Asp Trp Gly Phe Val Lys  
          165                 170                 175  
 Ala Ser Glu Gln Leu Gln Leu Ile Ile Asp Val Glu Glu Thr Thr Lys  
          180                 185                 190  
 Glu Asn Ser Arg Leu Gln Phe Ile Val Ala Leu Ser Tyr Ser Gly Gln  
  195                 200                 205  
 Cys Asp Ile Leu Gln Ala Cys Lys Asn Ile Gly His Lys Val Lys Asp  
  210                 215                 220  
 Gly Leu Ile Glu Pro Glu Asp Ile Asn Lys Ser Leu Ile Glu Gln Glu  
 225                 230                 235                 240  
 Leu Gln Thr Asn Cys Thr Glu Phe Pro Phe Pro Asp Leu Leu Ile Arg  
          245                 250                 255  
 Thr Ser Gly Glu Leu Arg Val Ser Asn Phe Met Leu Trp Gln Ile Ala  
  260                 265                 270  
 Tyr Thr Glu Leu Cys Phe Phe Ser Thr Leu Trp Pro Asp Phe Gly Lys  
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Asp Glu Phe Val Glu Ala Leu Ser Ser Phe Gln Lys Arg Gln Arg Arg  
 290 295 300

Tyr Gly Gly Arg Asn  
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 <212> DNA  
 <213> Oryza sativa

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 ggctctgggtc acaggggtggg cttctctgct ctcatgcca gcctgctcta ctgctatgaa 180  
 atgggctgta agtatatcac ggtgtatgca tttagcatcg ataattttaa gcgagatccg 240  
 actgaggtga aatccttgat ggagttaatg gaggaaaaga tcaatgaact gctagaaaac 300  
 agaaatgtca tcaacaaggt taactgtaag atcaacttct gggggaactt ggacatgttg 360  
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 aaggtctgtg cagaaaggag ggatatactg cagagggagg atgctgacag tgttgcaaat 540  
 aatggtgtgt attcagacat ttcagtggca gatctggacc gccatatgta cagcgctggg 600  
 tgccccgatc ctgacattgt gatccggacc tcaggtgaga ctgcctgag caatttcctt 660  
 ctgtggcaga cgacgttcag tcatttgtag aatccagacc ctctttggcc ggagtctctt 720  
 ttcaagcacc ttgtctgggc catactccag taccaaagag ttcacccttc tattgagcaa 780  
 agcagaaatc tggctaagaa gcagctgtaa tcacatcctc cctgggagga gatagaaacc 840  
 atcatacaag atatctgtag ttacacaata atctgtattc tcctgtggta tctcctggaa 900  
 tatgaaatat ataaaggata gctatgccat tgtatgcttg aacatgtgta tgcttgagtt 960  
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 a 1021

<210> 14  
 <211> 252  
 <212> PRT  
 <213> Oryza sativa

<400> 14  
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 Ala Leu Ile Ala Ser Leu Leu Tyr Cys Tyr Glu Met Gly Val Lys Tyr  
 35 40 45  
 Ile Thr Val Tyr Ala Phe Ser Ile Asp Asn Phe Lys Arg Asp Pro Thr  
 50 55 60  
 Glu Val Lys Ser Leu Met Glu Leu Met Glu Glu Lys Ile Asn Glu Leu  
 65 70 75 80  
 Leu Glu Asn Arg Asn Val Ile Asn Lys Val Asn Cys Lys Ile Asn Phe  
 85 90 95  
 Trp Gly Asn Leu Asp Met Leu Ser Lys Ser Val Arg Val Ala Ala Glu  
 100 105 110

Lys Leu Met Ala Thr Thr Ala Glu Asn Thr Gly Leu Val Phe Ser Val  
 115 120 125  
 Cys Met Pro Tyr Asn Ser Thr Ser Glu Ile Val Asn Ala Val Asn Lys  
 130 135 140  
 Val Cys Ala Glu Arg Arg Asp Ile Leu Gln Arg Glu Asp Ala Asp Ser  
 145 150 155 160  
 Val Ala Asn Asn Gly Val Tyr Ser Asp Ile Ser Val Ala Asp Leu Asp  
 165 170 175  
 Arg His Met Tyr Ser Ala Gly Cys Pro Asp Pro Asp Ile Val Ile Arg  
 180 185 190  
 Thr Ser Gly Glu Thr Arg Leu Ser Asn Phe Leu Leu Trp Gln Thr Thr  
 195 200 205  
 Phe Ser His Leu Gln Asn Pro Asp Pro Leu Trp Pro Glu Phe Ser Phe  
 210 215 220  
 Lys His Leu Val Trp Ala Ile Leu Gln Tyr Gln Arg Val His Pro Ser  
 225 230 235 240  
 Ile Glu Gln Ser Arg Asn Leu Ala Lys Lys Gln Leu  
 245 250

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 <213> *Oryza sativa*

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 gctgtcctct cgtatggccc aatgcctaag catattgcat ttattatgga tggtaaccgt 180  
 agatatgcta aattcaggag tatccaggaa ggctctgggtc acagggtggg cttctctgct 240  
 ctcattgcca gcctgctcta ctgctatgaa atgggcgtga agtatatcac ggtgtatgca 300  
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 atcaacttct ggggggaactt ggacatgttg agcaaatacag tgagggttagc agctgagaaa 480  
 ctgatggcta ccaactgctga aaacacggga ctggtcttct ctgtttgcat gccatacaac 540  
 tccacttctg agattgtcaa tgcggtcaat aagggtctgtg cagaaaggag ggatatactg 600  
 cagagggagg atgctgacag tgttgccaat aatgggtgtg attcagacat ttcagtggca 660  
 gatctggacc gccatatgta cagcgctggt tgccccgatc ctgacattgt gatccggacc 720  
 tcaggtgaga ctgcgctgag caatttcctt ctgtggcaga cgacgttcag tcatttgcag 780  
 aatccagacc ctctttggcc ggagttctct ttcaagcacc ttgtctgggc catactccag 840  
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<210> 16  
 <211> 299  
 <212> PRT  
 <213> *Oryza sativa*

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 Asn Phe Ile Arg Lys Cys Ile Val Ala Val Leu Ser Tyr Gly Pro Met  
                   35                  40                  45  
 Pro Lys His Ile Ala Phe Ile Met Asp Gly Asn Arg Arg Tyr Ala Lys  
                   50                  55                  60  
 Phe Arg Ser Ile Gln Glu Gly Ser Gly His Arg Val Gly Phe Ser Ala  
                   65                  70                  75                  80  
 Leu Ile Ala Ser Leu Leu Tyr Cys Tyr Glu Met Gly Val Lys Tyr Ile  
                   85                  90                  95  
 Thr Val Tyr Ala Phe Ser Ile Asp Asn Phe Lys Arg Asp Pro Thr Glu  
                   100                  105                  110  
 Val Lys Ser Leu Met Glu Leu Met Glu Glu Lys Ile Asn Glu Leu Leu  
                   115                  120                  125  
 Glu Asn Arg Asn Val Ile Asn Lys Val Asn Cys Lys Ile Asn Phe Trp  
                   130                  135                  140  
 Gly Asn Leu Asp Met Leu Ser Lys Ser Val Arg Val Ala Ala Glu Lys  
                   145                  150                  155                  160  
 Leu Met Ala Thr Thr Ala Glu Asn Thr Gly Leu Val Phe Ser Val Cys  
                   165                  170                  175  
 Met Pro Tyr Asn Ser Thr Ser Glu Ile Val Asn Ala Val Asn Lys Val  
                   180                  185                  190  
 Cys Ala Glu Arg Arg Asp Ile Leu Gln Arg Glu Asp Ala Asp Ser Val  
                   195                  200                  205  
 Ala Asn Asn Gly Val Tyr Ser Asp Ile Ser Val Ala Asp Leu Asp Arg  
                   210                  215                  220  
 His Met Tyr Ser Ala Gly Cys Pro Asp Pro Asp Ile Val Ile Arg Thr  
                   225                  230                  235                  240  
 Ser Gly Glu Thr Arg Leu Ser Asn Phe Leu Leu Trp Gln Thr Thr Phe  
                   245                  250                  255  
 Ser His Leu Gln Asn Pro Asp Pro Leu Trp Pro Glu Phe Ser Phe Lys  
                   260                  265                  270  
 His Leu Val Trp Ala Ile Leu Gln Tyr Gln Arg Val His Pro Ser Ile  
                   275                  280                  285  
 Glu Gln Ser Arg Asn Leu Ala Lys Lys Gln Leu  
                   290                  295

<210> 17  
 <211> 1028  
 <212> DNA  
 <213> Glycine max

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attctcacta ttatcactat cgttatcggt atcggttgta tcatcctttc catcacggtt 180
cccaaacaca gagtcttata gtctcgaagc gcggttccgc cattgcgaag tgtcacgctg 240
atagcgtgac acttcgtgat gacggagtct cgctcgcca agagtcgttg gagccacttc 300
cggcggaaact cgcggcggag atgatgccga agcatgtggc ggtgataatg gacgggaacg 360
ggaggtgggc gaaggtgaag gggctgccac catcggcggg gcaccaggcg ggggtgcaat 420
cgctgaggaa aatggtgagg ctgtgttgca gctggggaat taaggttcta acggttttcg 480
cgttctctac ggataactgg gttcgcccca aggtggaggt tgatttcttg atgaggctgt 540
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tgattggaga ttcatcaagg ttgcctgagt ctttaaaaag aatgatagct agtgcagaag 660
aggatacaaa acaaaattcg agattccaac ttattgtggc agtgggatac agtggaaaat 720
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tggatgacat aaacgaaaac attattgaac aagaattgga aactaattgt actgagtttc 840
cttatcctga tctactaata cgaactagtg gcgagcttag agtgagtaac ttcttggtgt 900
ggcaattagc ctacacagaa ctttatttta atcgggaact ctggccagat tttgggaagg 960
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attcataa 1028

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<210> 18
<211> 322
<212> PRT
<213> Glycine max

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Pro Ser Cys Tyr Tyr Ser His Tyr Tyr His Tyr Arg Tyr Arg Tyr Arg
          20             25             30

Cys Tyr His Pro Phe His His Arg Ser Gln Thr Gln Ser Leu Ile Val
          35             40             45

Ser Lys Arg Gly Ser Ala Ile Ala Lys Cys His Ala Asp Ser Val Thr
          50             55             60

Leu Arg Asp Asp Gly Val Ser Leu Ala Gln Glu Ser Leu Glu Pro Leu
          65             70             75             80

Pro Ala Glu Leu Ala Ala Glu Met Met Pro Lys His Val Ala Val Ile
          85             90             95

Met Asp Gly Asn Gly Arg Trp Ala Lys Val Lys Gly Leu Pro Pro Ser
          100            105            110

Ala Gly His Gln Ala Gly Val Gln Ser Leu Arg Lys Met Val Arg Leu
          115            120            125

Cys Cys Ser Trp Gly Ile Lys Val Leu Thr Val Phe Ala Phe Ser Thr
          130            135            140

Asp Asn Trp Val Arg Pro Lys Val Glu Val Asp Phe Leu Met Arg Leu
          145            150            155            160

Phe Glu Arg Thr Ile Asn Ser Glu Val Gln Thr Phe Lys Arg Glu Gly
          165            170            175

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Ile Arg Ile Ser Val Ile Gly Asp Ser Ser Arg Leu Pro Glu Ser Leu  
180 185 190

Lys Arg Met Ile Ala Ser Ala Glu Glu Asp Thr Lys Gln Asn Ser Arg  
195 200 205

Phe Gln Leu Ile Val Ala Val Gly Tyr Ser Gly Lys Tyr Asp Val Val  
210 215 220

Gln Ala Cys Lys Ser Val Ala Lys Lys Val Lys Asp Gly His Ile His  
225 230 235 240

Leu Asp Asp Ile Asn Glu Asn Ile Ile Glu Gln Glu Leu Glu Thr Asn  
245 250 255

Cys Thr Glu Phe Pro Tyr Pro Asp Leu Leu Ile Arg Thr Ser Gly Glu  
260 265 270

Leu Arg Val Ser Asn Phe Leu Leu Trp Gln Leu Ala Tyr Thr Glu Leu  
275 280 285

Tyr Phe Asn Arg Glu Leu Trp Pro Asp Phe Gly Lys Asp Glu Phe Val  
290 295 300

Asp Ala Leu Ser Ser Phe Gln Gln Arg Gln Arg Arg Tyr Gly Gly Arg  
305 310 315 320

His Ser

<210> 19

<211> 1026

<212> DNA

<213> Triticum aestivum

<400> 19

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gggaactcgc	ggtgggcggc	agcgcggggc	ctgccgccga	cggacgggca	cgagcacggg	180
atgcgcgcgc	tgatgaggac	ggtgcggctc	tcccgcgcct	ggggcatccg	cgtcctcacc	240
gccttcgggt	tctcgctcga	gaactggaat	cgccccaaag	cggaggttga	cttcttgatg	300
gccttgatcg	agaggtttat	caacgacaac	ctcgccgagt	tcttgaggga	agggacccgt	360
ctacgtataa	tcggtgaccg	ctcaaggctg	ccgatctctg	tcgagaagac	tcacagagac	420
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tcttgcccgg	acctgctcat	caggaccagc	ggcgagctga	ggctgagcaa	cttcctgcta	660
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gccccaatatc	tccaagccat	gatggccttc	cagagcagag	acaggcgctt	tggaagaaga	780
aaaaacaatg	cagcgctata	aataaacggt	gcacgcgcgt	gacccgatgc	tcgatcatcc	840
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<211> 266

<212> PRT

<213> Triticum aestivum

<400> 20

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      20              25              30

Arg His Val Ala Leu Val Met Asp Gly Asn Ser Arg Trp Ala Ala Ala
      35              40              45

Arg Gly Leu Pro Pro Thr Asp Gly His Glu His Gly Met Arg Ala Leu
      50              55              60

Met Arg Thr Val Arg Leu Ser Arg Ala Trp Gly Ile Arg Val Leu Thr
      65              70              75              80

Ala Phe Gly Phe Ser Leu Glu Asn Trp Asn Arg Pro Lys Ala Glu Val
      85              90              95

Asp Phe Leu Met Ala Leu Ile Glu Arg Phe Ile Asn Asp Asn Leu Ala
      100             105             110

Glu Phe Leu Arg Glu Gly Thr Arg Leu Arg Ile Ile Gly Asp Arg Ser
      115             120             125

Arg Leu Pro Ile Ser Val Gln Lys Thr Ala Arg Asp Ala Glu Glu Ala
      130             135             140

Thr Arg Asn Asn Ser Gln Leu Asp Leu Val Leu Ala Ile Ser Tyr Ser
      145             150             155             160

Gly Arg Met Asp Ile Val Gln Ala Cys Arg Asn Leu Ala Gln Lys Val
      165             170             175

Asp Ala Lys Leu Leu Arg Pro Glu Asp Ile Asp Glu Ser Leu Phe Ala
      180             185             190

Asp Glu Leu Gln Thr Ser Glu Thr Ser Cys Pro Asp Leu Leu Ile Arg
      195             200             205

Thr Ser Gly Glu Leu Arg Leu Ser Asn Phe Leu Leu Trp Gln Ser Ala
      210             215             220

Tyr Ser Glu Leu Phe Phe Thr Asp Thr Leu Trp Pro Asp Phe Gly Glu
      225             230             235             240

Ala Gln Tyr Leu Gln Ala Met Met Ala Phe Gln Ser Arg Asp Arg Arg
      245             250             255

Phe Gly Arg Arg Lys Asn Asn Ala Ala Leu
      260             265
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<210> 21

<211> 11

<212> PRT

<213> Artificial Sequence

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published alignment



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 <223> X = any amino acid

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 <223> X = any amino acid

<220>  
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 <222> (10)  
 <223> X = any amino acid

<300>  
 <301> Apfel, C. M.  
 <302> Use of Genomincs to Indentify Bacterial Undecaprenyl  
 Pyrophosphate Synthetase: Clooning, Expression, and  
 Characterization of the Essential uppS Gene  
 <303> J. Bacteriol.  
 <304> 81  
 <306> 483-492  
 <307> 1999

<400> 21  
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<210> 22  
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 <212> PRT  
 <213> Artificial Sequence

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<220>  
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<220>  
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<210> 23  
 <211> 750  
 <212> DNA  
 <213> Micrococcus luteus

<300>  
 <301> Shimizu, N.  
 <302> Molecular Cloning, Expression, and Purification of Undecprenyl  
         Diphosphate Synthase: No Sequence Similarity between E- and  
         Z-prenyl Diphosphate Synthases  
 <303> J. Biol. Chem.  
 <304> 273  
 <306> 19476-19481  
 <307> 1998

<400> 23  
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 aatgaatatt tatttacagc aaatatgcct gatcctgagt tgtaatcag aacttccggt 600  
 gaagaacgtt taagtaactt ttttaattgg caatgttcat atagtgagtt tgtatttata 660  
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<210> 24  
 <211> 249  
 <212> PRT  
 <213> Micrococcus luteus

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 Ala Ala Gln Ile Pro Lys His Ile Ala Ile Ile Met Asp Gly Asn Gly  
                           20                          25                          30  
 Arg Trp Ala Lys Gln Lys Lys Met Pro Arg Ile Lys Gly His Tyr Glu  
                           35                          40                          45  
 Gly Met Gln Thr Val Lys Lys Ile Thr Arg Tyr Ala Ser Asp Leu Gly  
           50                          55                          60  
 Val Lys Tyr Leu Thr Leu Tyr Ala Phe Ser Thr Glu Asn Trp Ser Arg

65		70		75		80
Pro Lys Asp Glu Val Asn Tyr Leu Met Lys Leu Pro Gly Asp Phe Leu						
	85			90		95
Asn Thr Phe Leu Pro Glu Leu Ile Glu Lys Asn Val Lys Val Glu Thr						
	100		105		110	
Ile Gly Phe Ile Asp Asp Leu Pro Asp His Thr Lys Lys Ala Val Leu						
	115		120		125	
Glu Ala Lys Glu Lys Thr Lys His Asn Thr Gly Leu Thr Leu Val Phe						
	130		135		140	
Ala Leu Asn Tyr Gly Gly Arg Lys Glu Ile Ile Ser Ala Val Gln Leu						
	145		150		155	160
Ile Ala Glu Arg Tyr Lys Ser Gly Glu Ile Ser Leu Asp Glu Ile Ser						
	165		170		175	
Glu Thr His Phe Asn Glu Tyr Leu Phe Thr Ala Asn Met Pro Asp Pro						
	180		185		190	
Glu Leu Leu Ile Arg Thr Ser Gly Glu Glu Arg Leu Ser Asn Phe Leu						
	195		200		205	
Ile Trp Gln Cys Ser Tyr Ser Glu Phe Val Phe Ile Asp Glu Phe Trp						
	210		215		220	
Pro Asp Phe Asn Glu Glu Ser Leu Ala Gln Cys Ile Ser Ile Tyr Gln						
	225		230		235	240
Asn Arg His Arg Arg Phe Gly Gly Leu						
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<210> 25  
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 <212> DNA  
 <213> *Saccharomyces cerevisiae*

<300>  
 <308> AB013497

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 ggggtacgca ttaaaattat cggcgatctc tctttgttgg ataagtctct attagaagat 420  
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 ccttttagatt tattgattag gacaagtggc gtttccagat taagtgactt tttgatattg 660  
 caggcatcga gtaagggcgt acgcatcgaa ttgctggatt gtttatggcc agagtttggg 720  
 cctatacggg taggcatggat tttattaaaa ttttcgtttc acaaatacct ttttaacaaa 780  
 gagtacagat tagaggaagg tgattatgac gaggaaccca atgggggaccc catcgatttg 840  
 aaagaaaaaa agttgaatta a 861

<210> 26  
 <211> 286  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 26  
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 Thr Lys Asn Ile Phe Ser Arg Thr Leu Arg Ala Ser Asn Cys Val Pro  
           20                  25                  30  
 Arg His Val Gly Phe Ile Met Asp Gly Asn Arg Arg Phe Ala Arg Lys  
           35                  40                  45  
 Lys Glu Met Asp Val Lys Glu Gly His Glu Ala Gly Phe Val Ser Met  
           50                  55                  60  
 Ser Arg Ile Leu Glu Leu Cys Tyr Glu Ala Gly Val Asp Thr Ala Thr  
           65                  70                  75                  80  
 Val Phe Ala Phe Ser Ile Glu Asn Phe Lys Arg Ser Ser Arg Glu Val  
                   85                  90                  95  
 Glu Ser Leu Met Thr Leu Ala Arg Glu Arg Ile Arg Gln Ile Thr Glu  
           100                  105                  110  
 Arg Gly Glu Leu Ala Cys Lys Tyr Gly Val Arg Ile Lys Ile Ile Gly  
           115                  120                  125  
 Asp Leu Ser Leu Leu Asp Lys Ser Leu Leu Glu Asp Val Arg Val Ala  
           130                  135                  140  
 Val Glu Thr Thr Lys Asn Asn Lys Arg Ala Thr Leu Asn Ile Cys Phe  
           145                  150                  155                  160  
 Pro Tyr Thr Gly Arg Glu Glu Ile Leu His Ala Met Lys Glu Thr Ile  
                   165                  170                  175  
 Val Gln His Lys Lys Gly Ala Ala Ile Asp Glu Ser Thr Leu Glu Ser  
                   180                  185                  190  
 His Leu Tyr Thr Ala Gly Val Pro Pro Leu Asp Leu Leu Ile Arg Thr  
           195                  200                  205  
 Ser Gly Val Ser Arg Leu Ser Asp Phe Leu Ile Trp Gln Ala Ser Ser  
           210                  215                  220  
 Lys Gly Val Arg Ile Glu Leu Leu Asp Cys Leu Trp Pro Glu Phe Gly  
           225                  230                  235                  240  
 Pro Ile Arg Met Ala Trp Ile Leu Leu Lys Phe Ser Phe His Lys Ser  
                   245                  250                  255  
 Phe Leu Asn Lys Glu Tyr Arg Leu Glu Glu Gly Asp Tyr Asp Glu Glu  
           260                  265                  270  
 Thr Asn Gly Asp Pro Ile Asp Leu Lys Glu Lys Lys Leu Asn  
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<210> 27  
 <211> 1032  
 <212> DNA  
 <213> *Saccharomyces cerevisiae*

<300>  
 <308> AB013498

<400> 27  
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 atgtcattaa gcttggttttc atgggttttat gtaaatcttc agaataattt gataaaagca 180  
 ttaagggttag ggccagtgcc tgaacatgtc tcctttatca tggatggtaa ccggagatat 240  
 gccaagtcaa gaaggctacc agtaaaaaaa ggccatgaag ctgggtgggtt aacgttacta 300  
 aactactgtg atatctgcaa aagattgggt gtaaaatgtg tttccgccta tgcattttct 360  
 attgaaaatt ttaatagacc aaaagaagaa gtagatacgc taatgaattt gtttacggta 420  
 aagcttgatg aattcgcaaa aagagccaag gactataagg atcccttata cggatctaaa 480  
 ataagaatag taggtgatca atctttacta tctccagaaa tgagaaaaaa aattaaaaaa 540  
 gtggaagaaa tcacacagga tggagacgat ttcactttat ttatatgttt tccttacct 600  
 tcaagaaatg atatgttaca tactattcgt gattcagttg aagaccattt ggaaaaataaa 660  
 tcaccaagga ttaatataga aaaatttact aataaaatgt acatgggttt ccattccaat 720  
 aaatgtgaat tattaatcag aacaagtggg cataggaggc tctcagacta tatgctatgg 780  
 caagtacatg aaaatgccac cattgaattt agtgatacgt tgtggccaaa ttttagcttc 840  
 tttgctatgt acctgatgat tctcaaattg tccttctttt ccaccattca aaaatataat 900  
 gagaagaatc actcattgtt tgaaaaaata catgaaagcg ttccttcaat atttaaaaaa 960  
 aagaaaacag ctatgtcttt gtacaacttt ccaaaccctt ccatttcagt ttcggttaca 1020  
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<210> 28  
 <211> 343  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 28  
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 Phe Gln Arg Val Phe Ala Trp Val Met Ser Leu Ser Leu Phe Ser Trp  
 35 40 45  
 Phe Tyr Val Asn Leu Gln Asn Ile Leu Ile Lys Ala Leu Arg Val Gly  
 50 55 60  
 Pro Val Pro Glu His Val Ser Phe Ile Met Asp Gly Asn Arg Arg Tyr  
 65 70 75 80  
 Ala Lys Ser Arg Arg Leu Pro Val Lys Lys Gly His Glu Ala Gly Gly  
 85 90 95  
 Leu Thr Leu Leu Thr Leu Leu Tyr Ile Cys Lys Arg Leu Gly Val Lys  
 100 105 110  
 Cys Val Ser Ala Tyr Ala Phe Ser Ile Glu Asn Phe Asn Arg Pro Lys  
 115 120 125  
 Glu Glu Val Asp Thr Leu Met Asn Leu Phe Thr Val Lys Leu Asp Glu  
 130 135 140

Phe Ala Lys Arg Ala Lys Asp Tyr Lys Asp Pro Leu Tyr Gly Ser Lys  
 145 150 155 160  
 Ile Arg Ile Val Gly Asp Gln Ser Leu Leu Ser Pro Glu Met Arg Lys  
 165 170 175  
 Lys Ile Lys Lys Val Glu Glu Ile Thr Gln Asp Gly Asp Asp Phe Thr  
 180 185 190  
 Leu Phe Ile Cys Phe Pro Tyr Thr Ser Arg Asn Asp Met Leu His Thr  
 195 200 205  
 Ile Arg Asp Ser Val Glu Asp His Leu Glu Asn Lys Ser Pro Arg Ile  
 210 215 220  
 Asn Ile Arg Lys Phe Thr Asn Lys Met Tyr Met Gly Phe His Ser Asn  
 225 230 235 240  
 Lys Cys Glu Leu Leu Ile Arg Thr Ser Gly His Arg Arg Leu Ser Asp  
 245 250 255  
 Tyr Met Leu Trp Gln Val His Glu Asn Ala Thr Ile Glu Phe Ser Asp  
 260 265 270  
 Thr Leu Trp Pro Asn Phe Ser Phe Phe Ala Met Tyr Leu Met Ile Leu  
 275 280 285  
 Lys Trp Ser Phe Phe Ser Thr Ile Gln Lys Tyr Asn Glu Lys Asn His  
 290 295 300  
 Ser Leu Phe Glu Lys Ile His Glu Ser Val Pro Ser Ile Phe Lys Lys  
 305 310 315 320  
 Lys Lys Thr Ala Met Ser Leu Tyr Asn Phe Pro Asn Pro Pro Ile Ser  
 325 330 335  
 Val Ser Val Thr Gly Asp Glu  
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<210> 29

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 29

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32

<210> 30

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 30  
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<210> 31  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<400> 31  
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<210> 32  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<400> 32  
 ttgagctcta tctcctccca gggagg 26

<210> 33  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<400> 33  
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<210> 34  
 <211> 26  
 <212> DNA  
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<220>  
 <223> Description of Artificial Sequence:primer

<400> 34  
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<210> 35  
 <211> 37  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 35

ctagtctaga atctcccctc cgataaccaa aaaatcc

37

<210> 36

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 36

ggggtaccta ggggtttaact tagaaactat ttag

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<212> DNA

<213> arabidopsis

<400> 37

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aagaaaaact	tcattctctt	gtttatatatt	cactcgcaac	aaaaaaaaaca	aaaaaaaaaca	180
aagtgtgttc	ttaaattatc	ttctctgata	acaaaaaaag	ccctattttc	cgagatgaat	240
accctagaag	aagtagatga	atccactcat	atcttcaacg	ctttgatgag	tctaatagagg	300
aaatttttgt	tcagagttct	atgcgtcggg	ccaatcccta	ctaacatttc	attcatcatg	360
gatggaaacc	gcaggttcgc	taagaaacac	aatcttatag	gcctagatgc	aggacataga	420
gctggtttca	tatccgtgaa	atatattctt	caatactgca	aagagattgg	tgtaccgtac	480
gtcacactcc	acgcgtttgg	tatggataat	ttcaagagag	gacctgaaga	agtcaagtgt	540
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atgaacggcg	tgagaataat	ctttgccggg	gattttggatt	cgttaaacga	gcatttttaga	660
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